

SEQUENCE LISTING

<110> The Chemo-Sero-Therapeutic Research Institute

<120> A DNA coding for merozoite protein of Babesia caballi, a recombinant protein obtained by using said DNA and a use thereof

<130> 661440

<160> 2

<210> 1

<211> 1828

<212> DNA

<213> Babesia caballi

<400> 1

GTGCCTGGC CGTTCGCCAC AACAGCCGTG TTTCCATC ATG GCT CCC AGC GAC TCT	56
Met Ala Pro Ser Asp Ser	
1 5	
GTG GGC GAC GTG ACT AAG ACC TTA TTG GCT GCC AGC GAA AGT GTG GAC	104
Val Gly Asp Val Thr Lys Thr Leu Leu Ala Ala Ser Glu Ser Val Asp	
10 15 20	
TCA GCT GCC AAT GCC TAT ATG ATC AAC AGT GAC ATG AGC GAT TAC TTG	152
Ser Ala Ala Asn Ala Tyr Met Ile Asn Ser Asp Met Ser Asp Tyr Leu	
25 30 35	
TCG GCT GTG TCT GAC AAC TTC GCC GAG CGC ATT TGC AGT CAG GTC CCT	200
Ser Ala Val Ser Asp Asn Phe Ala Glu Arg Ile Cys Ser Gln Val Pro	
40 45 50	
AAG GGG AGT AAC TGC AGT GCT TCC GTT AGC GCA TAC ATG AGT CGC TGC	248
Lys Gly Ser Asn Cys Ser Ala Ser Val Ser Ala Tyr Met Ser Arg Cys	
55 60 65 70	
GCT AAA CAG GAC TGC CTG ACT CTC CAA AGT CTT AAG TAC CCT CTT GAG	296
Ala Lys Gln Asp Cys Leu Thr Leu Gln Ser Leu Lys Tyr Pro Leu Glu	
75 80 85	
GCT AAG TAC CAA CCG CTG ACC CTT CCT GAC CCC TAC CAG TTG GAG GCC	344
Ala Lys Tyr Gln Pro Leu Thr Leu Pro Asp Pro Tyr Gln Leu Glu Ala	
90 95 100	
GCA TTT ATA CTC TTC AAG GAG AGT GAC GCT AAT CCG GCC AAT AGC ACT	392
Ala Phe Ile Leu Phe Lys Glu Ser Asp Ala Asn Pro Ala Asn Ser Thr	
105 110 115	

GAG AAG CGC TTC TGG ATG CGT TTC AGA AGG GGC AAG AAC CAC AGT TAC	440
Glu Lys Arg Phe Trp Met Arg Phe Arg Arg Gly Lys Asn His Ser Tyr	
120 125 130	
TTC CAC GAC TTA GTC TTC AAT CTG CTG GAG AAG AAC GTG ACT CGC GAC	488
Phe His Asp Leu Val Phe Asn Leu Leu Glu Lys Asn Val Thr Arg Asp	
135 140 145 150	
GCG GAT GCT ACT GAC ATT GAG AAC TTT GCG TCC AGG TAC CTG TAC ATG	536
Ala Asp Ala Thr Asp Ile Glu Asn Phe Ala Ser Arg Tyr Leu Tyr Met	
155 160 165	
GCC ACG CTT TAC TAC AAG ACG TAC ACG AAT GTT GAT GAG TTC GGT GCT	584
Ala Thr Leu Tyr Tyr Lys Thr Tyr Thr Asn Val Asp Glu Phe Gly Ala	
170 175 180	
AGC TTC TTT AAC AAG TTG TCT TTC ACT ACT GGG TTG TTC GGC TGG GGC	632
Ser Phe Phe Asn Lys Leu Ser Phe Thr Thr Gly Leu Phe Gly Trp Gly	
185 190 195	
ATC AAG AGG GCA CTT AAG CAG ATT ATT CGC TCT AAC CTG CCC CTT GAC	680
Ile Lys Arg Ala Leu Lys Gln Ile Ile Arg Ser Asn Leu Pro Leu Asp	
200 205 210	
ATC GGG ACA GAA CAC AGC GTC AGT CGC CTG CAG CAC ATT ACG AGC AGT	728
Ile Gly Thr Glu His Ser Val Ser Arg Leu Gln His Ile Thr Ser Ser	
215 220 225 230	
TAC AAG GAT TAC ATG GAT ACG CAG ATT CCT GCA CTG CCC AAG TTT GCG	776
Tyr Lys Asp Tyr Met Asp Thr Gln Ile Pro Ala Leu Pro Lys Phe Ala	
235 240 245	
AAG CGT TTC TCC CTT ATG GTA GTG CAG AGG CTG CTG GCC ACC GTG GCT	824
Lys Arg Phe Ser Leu Met Val Val Gln Arg Leu Leu Ala Thr Val Ala	
250 255 260	
GGT TAC GTC GAC ACC CCG TGG TAT AAG AAG TGG TAC ATG AAG CTG AAG	872
Gly Tyr Val Asp Thr Pro Trp Tyr Lys Lys Trp Tyr Met Lys Leu Lys	
265 270 275	
AAC TTT ATG GTG AAC AGG GTG TTC ATT CCT ACA AAG AAG TTC TTC AAT	920
Asn Phe Met Val Asn Arg Val Phe Ile Pro Thr Lys Lys Phe Phe Asn	
280 285 290	
AAG GAA ATT CGT GAG CCT AGT AAG GCA TTA AAA GAA AAG GTG TCA ACC	968
Lys Glu Ile Arg Glu Pro Ser Lys Ala Leu Lys Glu Lys Val Ser Thr	
295 300 305 310	

GAC ACC AAG GAT TTA TTC GAG AAC AAA ATT GGG CAG GGT ACT GTG GAC 1016
 Asp Thr Lys Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp
 315 320 325
 TTC TTC AAT AAG GAA ATT CGT GAC CCT AGT AAG GCA TTA AAA GAA AAA 1064
 Phe Phe Asn Lys Glu Ile Arg Asp Pro Ser Lys Ala Leu Lys Glu Lys
 330 335 340
 GTG TCA AAC GAC GCC AAG GAT TTA TTC GAG AAC AAA ATT GGG CAG GGT 1112
 Val Ser Asn Asp Ala Lys Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly
 345 350 355
 ACT GTG GAC TTC ATC AAT AAC GAA ATT CGT GAC CCT AGT AAG GCA TTA 1160
 Thr Val Asp Phe Ile Asn Asn Glu Ile Arg Asp Pro Ser Lys Ala Leu
 360 365 370
 ATA AGA AAA GTG TCA ACG GGG GCC GAG GAT TTA TTC GAG AAC AAA ATT 1208
 Ile Arg Lys Val Ser Thr Gly Ala Glu Asp Leu Phe Glu Asn Lys Ile
 375 380 385 390
 GGG CAG GGT ACT GTG GAC TTC ATC AAT AAC GAA ATT CGT GAC CCT AGT 1256
 Gly Gln Gly Thr Val Asp Phe Ile Asn Asn Glu Ile Arg Asp Pro Ser
 395 400 405
 AAG GCA TTA ATA AGA AAA GTG TAC ACC GAG GCC GAT GAT TTA TTC GAG 1304
 Lys Ala Leu Ile Arg Lys Val Tyr Thr Glu Ala Asp Asp Leu Phe Glu
 410 415 420
 AAC AAA ATT GGG CAG GGT ACT GTG GAC TTC ATC AAT AAG GAA ATT CGT 1352
 Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Lys Glu Ile Arg
 425 430 435
 GAC CCT AGT AAG GCA TTA ATA AGA AAA GTG TCT ACC GAG GCC GAT AAT 1400
 Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Ser Thr Glu Ala Asp Asn
 440 445 450
 TTA TTG GAG AAA TAGGTTGCGA AGCCCTGAG GAAGCACCGC AAGGGCAACG TTAGT 1457
 Leu Leu Glu Lys
 455
 GACAGCGGGG AATCTGAGGA AATTTGCGCT GTGGGTGAAT CTTTGGAATC CGACAACGAA 1517
 ATGAAGACCC AGGAGTCAAT GAACTCGGAG AGTGCTTCTA CCGAACTCCC TTCTGAGGAG 1577
 TCCGAGGAAG AGTCGGCTGC TATGTTTATT CAGCAGCCCA CCCTGGAGGA GGCCAGCCAG 1637
 ATCGCATTGC CTGCTGAAGA AGACAGCTCA GAGTTGCAGG AAACCTCCGA CAACTATGAA 1697
 GCCTCTCTCT AGTCACCTTT GACGTCCATC GCACTGCTCG GAGAATATAA AACGCATTGC 1757
 TCGGTTGCAC TCTAGTTGTT AACAATGCAC AATTTAATGT TATAGTTGTT TTGAAAAAAA 1817